

GenCore version 4.5  
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Allele D4.7 of the  
Recombinant human

#### OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 11:24:48 ; search time 134.55 Seconds

(without alignments)  
923.880 Million cell updates/sec

Title: US-08-956-991-1  
Perfect score: 6504  
Sequence: 1 tqactqaggccgagcacgg. .... gaaatggccaaatatt 6504

Scoring table: IDENTITY\_NUC

Searched: 240622 seqs, 94055609 residues

Database : N\_Geneseq\_34 : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID
------------	-------	-------	-------	--------	----	----

Description	
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PI	Korenberg, JR;
----	----------------

DR

WPI, 98-21791/24.

P-PSDB; W42086.

PT New isolated Down's Syndrome-cell adhesion molecule - used to develop products for detection, diagnosis and therapy of developmental and neurological abnormalities

PT

CC



OM nucleic - nucleic search, using sw model  
Run on: July 23, 1999, 11:23:48 ; search time 73.57 Seconds  
(without alignments)  
Perfect score: 6604  
Sequence: 1 tqactgagggcgqgacqg.....gaaaattqccaaatatt 6604  
Scoring table: IDENTITY\_NUC  
Searched: 176461 seqs, 45838279 residues

C	38	53.4	0.8	2483	5	PCU-USDA-08449A-3	Sequence 3, Appli
C	39	53.2	0.8	1335	5	PCU-USDA-08432-1	Sequence 1, Appli
C	40	53	0.8	6407	4	US-08-161-8434-7	Sequence 7, Appli
C	41	53	0.8	6407	4	US-08-599-554-7	Sequence 7, Appli
C	42	52.6	0.8	6407	4	US-08-18-937-4	Sequence 7, Appli
C	43	52.6	0.8	7011	3	US-08-305-991B-4	Sequence 4, Appli
C	44	52.6	0.8	4524	4	US-08-645-998-7	Sequence 4, Appli
C	45	52.4	0.8	2003	1	US-08-035-555B-21	Sequence 21, Appli

Query Match 1.0%; Score 56.4; DB 4; Length 6000;  
 Best Local Similarity 47.7%; Pred. No. 7; 5e-07;  
 Matches 227; Conservative 0; Mismatches 245; Indels 3; Gaps 1;  
 Ov 3597 tacaccctgqacaaccqataacttcactccqataacttcaatggccatqcttqatac 3656

RESULT 2  
 US-08-800-825A-5  
 Sequence 6, Application US/08800825A  
 ; Patent No. 5896397  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RODAN, GIDEON A.  
 ; SCHMIDT, AZRIEL  
 ; RUTLEDGE, SU JANE  
 ; CDNA ENCODING A NOVEL HUMAN PROTEIN  
 ; TYROSINE PHOSPHATASE  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
 ; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
 ; CITY: RAILWAY  
 ; STATE: NEW JERSEY  
 ; COUNTRY: USA  
 ; ZIP: 07055-0900  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/800, 825A  
 ; FILING DATE: 14-FEB-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HAND, J. MARK  
 ; REGISTRATION NUMBER: 36, 545  
 ; REFERENCE DOCKET NUMBER: 18992DA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 732-594-3905  
 ; TELEFAX: 732-594-4720  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5000 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-800-825A-6

RESULT 3  
 PCT-US4-10166-6  
 Sequence 6, Application PC/US9410166  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RODAN, GIDEON A.  
 ; SCHMIDT, AZRIEL  
 ; RUTLEDGE, SU JANE  
 ; CDNA ENCODING A NOVEL HUMAN PROTEIN  
 ; TYROSINE PHOSPHATASE  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: JOHN W. WALLEN III  
 ; STREET: P. O. BOX 2000, 126 E. LINCOLN AVE.  
 ; CITY: RAILWAY  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07055  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/10166  
 ; FILING DATE: 09-SEPT-1994  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/122, 032  
 ; FILING DATE: 14-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WALLEN, JOHN W III  
 ; REGISTRATION NUMBER: 35403  
 ; REFERENCE DOCKET NUMBER: 18992  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 908-594-3905  
 ; TELEFAX: 908-594-4720  
 ; TELEX: 138825  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6000 base pairs  
 ; TYPE: nucleic acid

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OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 10:47:22 ; Search time 1887.56 Seconds

(Without alignments) 12516.755 Million cell updates/sec

Title: US-08-956-991-1  
Perfect score: 6604  
Sequence: 1 tgactqaggccggagacgg.....gaaaatttgc当地 6604

Scoring table: IDENTITY\_NUC  
Searched: 808301 seqs, 1788773984 residues

Database: GenEmpl: \*  
1: gb\_bal: \*  
2: gb\_ba2: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_p11: \*  
9: gb\_p12: \*  
10: gb\_p11: \*  
11: gb\_pr2: \*  
12: gb\_pr1: \*  
13: gb\_xo: \*  
14: gb\_st: \*  
15: gb\_sy: \*  
16: gb\_un: \*  
17: gb\_v1: \*  
18: gb\_htg: \*  
19: em\_bai: \*  
20: em\_fun: \*  
21: em\_hum: \*  
22: em\_hum2: \*  
23: em\_in: \*  
24: em\_om: \*  
25: em\_or: \*  
26: em\_ov: \*  
27: em\_pat: \*  
28: em\_ph: \*  
29: em\_p1: \*  
30: em\_ro: \*  
31: em\_sy: \*  
32: em\_un: \*  
33: em\_v1: \*  
34: em\_htg: \*  
35: em\_sts: \*  
36: gb\_bai: \*  
37: gb\_bai: \*  
38: gb\_ba2: \*  
39: gb\_ba1: \*  
40: gb\_p12: \*  
41: gb\_p11: \*  
42: gb\_pr2: \*  
43: gb\_pr3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
------------	-------	--------------	-------	-------------

RESULT	1	AF023450	6212	94.1	6413	11	AF023450
LOCUS	AF023450	6413 bp	6212	94.1	6413	42	AF023450
DEFINITION	Homo sapiens CHD2-52 Down syndrome cell adhesion molecule (DSCAM)	mRNA	6110	92.5	6110	11	Homo sapi
ACCESSION	AF023450	mRNA, complete cds.	6110	92.5	6110	42	AF023449
NID	93169767		699	10.6	721	11	AF023449
KEYWORDS	human		699	10.6	721	11	AF023449
SOURCE	Homo sapiens		721	42	HUM291F03		AF023449
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		721	42	AF023450		AF023450
REFERENCE	1 (bases 1 to 6413)		721	42	AF023450		Homo sapi
AUTHORS	Kanakava, K., Huo, Y.-K., Haendel, M.A., Hubert, R., Chen, X.-N., Lyons, G.E. and Korenberg, J.R.		721	42	AF023450		AF023450
TITLE	DSCAM: a Novel Member of the Immunoglobulin Superfamily Maps in a Down Syndrome Region and is Involved in the Development of the Nervous System		721	42	AF023450		Homo sapi
JOURNAL	Unpublished		721	42	AF023450		AF023450
REFERENCE	2 (bases 1 to 6413)		721	42	AF023450		SHGC-3033
AUTHORS	Yamaka, K., Huo, Y.-K., Haendel, M.A., Hubert, R., Chen, X.-N., Lyons, G.E. and Korenberg, J.R.		721	42	AF023450		AF023450
TITLE	Direct Submission		721	42	AF023450		AF023450

## ALIGNMENTS

RESULT	1	AF023450	6212	94.1	6413	11	AF023450
LOCUS	AF023450	6413 bp	6212	94.1	6413	42	AF023450
DEFINITION	Homo sapiens CHD2-52 Down syndrome cell adhesion molecule (DSCAM)	mRNA	6110	92.5	6110	11	Homo sapi
ACCESSION	AF023450	mRNA, complete cds.	6110	92.5	6110	42	AF023449
NID	93169767		699	10.6	721	11	AF023449
KEYWORDS	human		699	10.6	721	11	AF023449
SOURCE	Homo sapiens		721	42	HUM291F03		AF023449
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		721	42	AF023450		AF023450
REFERENCE	1 (bases 1 to 6413)		721	42	AF023450		Homo sapi
AUTHORS	Kanakava, K., Huo, Y.-K., Haendel, M.A., Hubert, R., Chen, X.-N., Lyons, G.E. and Korenberg, J.R.		721	42	AF023450		AF023450
TITLE	DSCAM: a Novel Member of the Immunoglobulin Superfamily Maps in a Down Syndrome Region and is Involved in the Development of the Nervous System		721	42	AF023450		AF023450
JOURNAL	Unpublished		721	42	AF023450		AF023450
REFERENCE	2 (bases 1 to 6413)		721	42	AF023450		SHGC-3033
AUTHORS	Yamaka, K., Huo, Y.-K., Haendel, M.A., Hubert, R., Chen, X.-N., Lyons, G.E. and Korenberg, J.R.		721	42	AF023450		AF023450
TITLE	Direct Submission		721	42	AF023450		AF023450

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Run on: July 23, 1999, 10:47:22 : Search time 1887.56 seconds

(without alignments)

12516.755 Million cell updates/sec

Title: US-08-956-991-1  
Perfect score: 6604  
Sequence: 1 tggatggccggagcacqg . . . . . gaaaattggccaaatataatt 6604

Scoring table: IDENTITY\_NUC

Searched: 808301 seqs, 1788773984 residues

Database : GenEmbl:\*

gb\_bail:\*

gb\_ba2:\*

gb\_in:\*

gb\_om:\*

gb\_ov:\*

gb\_pat:\*

gb\_ph:\*

gb\_ps1:\*

gb\_ps2:\*

gb\_st:\*

gb\_sy:\*

gb\_tp2:\*

gb\_tp3:\*

gb\_rop:\*

gb\_stc:\*

gb\_sty:\*

gb\_tp1:\*

gb\_tp2:\*

gb\_tp3:\*

gb\_tp4:\*

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gb



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OM nucleic - nucleic search, using sw model

Run on: July 23, 1999, 09:42:16 : Search time 795.19 Seconds  
 (without alignments)  
 12668.548 Million cell updates/sec

Scoring table: IDENTITY\_NUC

Searched: 202476 seqs, 762712212 residues

Perfect score: 6604  
 Sequence: 1 tgactggagcgccggacagg.....gaaaattgcacaaatattt 6604

base : EST:\*

1: em\_est1:\*

2: em\_est2:\*

3: em\_est3:\*

4: em\_est4:\*

5: em\_est5:\*

6: em\_est6:\*

7: em\_est7:\*

8: em\_est8:\*

9: em\_est9:\*

10: qb\_est1:\*

11: qb\_est2:\*

12: qb\_est3:\*

13: qb\_est4:\*

14: qb\_est5:\*

15: qb\_est6:\*

16: qb\_est7:\*

17: qb\_est8:\*

18: qb\_est9:\*

19: qb\_est10:\*

20: qb\_est11:\*

21: qb\_est12:\*

22: qb\_est13:\*

23: qb\_est14:\*

24: qb\_est15:\*

25: qb\_est16:\*

26: qb\_est17:\*

27: qb\_est18:\*

28: qb\_est19:\*

29: qb\_est20:\*

30: qb\_est21:\*

31: qb\_est22:\*

32: qb\_est23:\*

33: qb\_est24:\*

34: qb\_est25:\*

35: qb\_est26:\*

36: qb\_est27:\*

37: qb\_est28:\*

38: qb\_est29:\*

39: qb\_est30:\*

40: qb\_est31:\*

41: qb\_est32:\*

42: qb\_est33:\*

43: qb\_est34:\*

44: qb\_est35:\*

45: qb\_est36:\*

46: qb\_est37:\*

47: qb\_est38:\*

48: qb\_est39:\*

49: qb\_est40:\*

50: qb\_est41:\*

51: qb\_est42:\*

52: qb\_est43:\*

53: qb\_est44:\*

54: qb\_est45:\*

55: qb\_est46:\*

56: qb\_est47:\*

57: qb\_est48:\*

58: qb\_est49:\*

59: qb\_est50:\*

60: qb\_est51:\*

61: qb\_est52:\*

62: qb\_est53:\*

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64: qb\_est55:\*

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112: qb\_est103:\*

113: qb\_est104:\*

114: qb\_est105:\*

115: qb\_est106:\*

116: qb\_est107:\*

117: qb\_est108:\*

118: qb\_est109:\*

119: qb\_est110:\*

120: qb\_est111:\*

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 453 ATGTCGATACTGSCCTCTCTGTTCCAGAGCTTCCGAATGTTTCAG 502  
 17 rGlusPheLeuIleSerSerLeuIlePheAlaAsnAlaSerLeuGly 34  
 ||||||| 503 TGAGGACTTACACTCCAGCTCTACTTGTCAATGCACTCTGCAAGAGG 552  
 34 alvalPheAlaSerSerLeuIlePheAlaAsnAlaSerLeuGly 50  
 ||||||| 553 TAGTTTGCCAGCACCACGGGACTCTGCTGCCAGGGCAGAGCTGA 602  
 67 rAspIleProGlyIleLeuIleArgTrpIleLeuIlePheAlaAsnAla 67  
 ||||||| 553 CGATGTCGCCCGGATCGCCAGTCACCCCAACGGCACTTCGGCAAT 702  
 84 heProIleProProSerSerPheSerSerThrLeuIleHisAsnProAsnGlyThrLeuIlePhe 84  
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 101 TYRCYSthrAlaGluAsnProSerGlyLysIleArgSerGlnAspValH 117  
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 317 rIleSerProArgLysValLysSerSerValGlySerGlnValSerIeus 334  
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 334 eCysSerValThrGlyLysGluAspGlyInleIleUserAspTrpIleGly 350  
 1453 CCTGCAGCGGAGCACTGAGGACGAGCACTCCCTGTTACCGCAAT 1502  
 351 GlyGluIleLeuAspProGlyLysValArgIleIleGlyIleAsnI 367  
 1503 GGTGAATTCCTCACCCCTGGAAATAATGAGATCACAGGGTCACCA 1552  
 367 sIleAspLeuIleMetAspHisMetValLysSerAspGlyLysIleIle 384  
 1603 ATGCTTGTGCGCAGACGCTCTCCGCTCAAGACTATGTGAGGTG 1652  
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 1653 GTCCTGAGATGGAATCCTCAAATTATTCCTGCTTGTGAAAGGT 1702  
 417 IleValSerProAlaIleGluIleValSerIleMetCysAsnValYsGly 434  
 1703 GGAGTCAGGAGAGCGGTTCCCTATGCGCTGAGCTGAGGAC 1752  
 434 rIleLeuProThrIleIleTrpIleLeuAspAspProIleLeuIleGly 450  
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 451 GlySerHisArgIleSerGlyIleIleIleIleIleIleIleIle 467  
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 1853 CTACTGTGACATCTCCACCTCCAGGTCAGTCGGACGGGAGCTACCGCT 1902  
 484 ysthreAlaAsnAsnSerAlaIleGlyValValLeuIleTyrglyAlaIleAsn 500  
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 501 ValArgGlyProAlaSerIleIleArgProIleIleIleIleIleIle 517  
 1953 GTAGAGGGCTGGCAGATTGACCATGATGAAACATCACAGCAATAGC 2002  
 517 aGlyIleArgAspThrIleIleHisCysArgValIleIleGlyIlePheAspH 534  
 2003 AGGACGGGACACATCACATCACGTCGCTGTGATGGCTATCCGTATACT 2052  
 534 erIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 550  
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 584 erThrSerGlySerValHisValIleValIleValIleProProPheIleGly 600  
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 601 ProPheIlePheProArgPheSerIleIleGlyIleGlyIleGlyIlePro 617

OM of: US-08-956-991-2 to: Issued\_Patents\_NA.\* out\_format : pfs

Date: Jul 23, 1999 12:09 PM

About: Results were produced by the Gencore software, version 4.5, Copyright (c) 1993-1998 Comigen Ltd.

#### Command line parameters:

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-MODEL:frame+>p20.model -DEV=x1P
-Q=/cgn2_6/podata/2/ina/PCTUS9.spool/US08956991/runat_23071999_094001_14124/app_query.fasta.1
-DB=issued_Patents_NA -OFMT=fastaP -SUFFIX=rml -GAPR=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPBL=0.000 -LOOPEXT=0.000
-OGAPR=4.500 -OGAPEXT=0.050 -XGAPR=10.000 -XGAPEXT=0.500
-FGAPR=6.000 -FGAPEXT=7.000 -YGAPR=10.000 -YGAPEXT=0.500
-DELG=6.000 -DELEX=7.000 -START=1 -MATRIX=am150
-TRANS=human40.001 -LIST=45 -DOCALIGN=200 -THR_SCORE=escore
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=stat -USER=US08956991
-NCPU=6 -ICLU=3 -WAIT -THREADS=1
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#### Search information block:

Query: US-08-956-991-2

Query length: 1910

Database: Issued\_Patents\_NA.\*

Database length: 176451

Search time (sec): 53.630000

score\_list:

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seq\_name: /cgn2\_6/podata/2/ina/PCTUS9\_COMB.seq:PCT-US94-05277-1

seq\_documentation\_block:

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Sequence 1, Application PCT-US94-05277

GENERAL INFORMATION:

APPLICANT: Bruskin, Arthur

APPLICANT: Jarosz, David E.

APPLICANT: Kinzler, Kenneth W.

APPLICANT: Vogelstein, Bert

APPLICANT: Zabrecky, James R.

TITLE OF INVENTION: Antibodies Specific for DCC Gene Product

NUMBER OF SEQUENCES: 2

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CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT-US94-05277  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202.508.9100  
TELEFAX: 202.508.9299  
TELEX: 197430 BBMB UT

SEQUENCE CHARACTERISTICS:  
SEQUENCE LENGTH: 4608 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 18q21

FEATURES:

NAME/KEY: CDS

LOCATION: 1..4342

PCT-US94-05277-1

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Quality: 653.00

Length: 1326

Ratio: 0.918

Gaps: 51

Percent Similarity: 53.620

Identity: 24.133

alignment\_block:

PCT-US94-05277-1 ..

05-08-956-991-2 x PCT-US94-05277-1 ..

Align seg 1/1 to: PCT-US94-05277-1 from: 1 to: 4608

535 IleLysTyrProTyrLysAsnSerAsnLeuLeuProPhe....AsnHisAR 549

214 ATGAGTGGAGAAGATGGCTTCAGCTGGCTTGGAGTGGAGAAG 253

